O'Bryen, Barbara

From:

Switzer, Juliet

Sent:

Wednesday, February 09, 2005 4:05 PM

To: Subject: O'Bryen, Barbara FW: please search

here's the sequence of I want searched:

iaaaiatgctctgtrtatatgctataiggi

the case is CRIFE but not in AIBSS b/c the CRIF is too big. you'd have to go get the CD from mark spencer, but I've already OCRed the sequence. Thanks.

-----Original Message-----

From:

Switzer, Juliet

Sent:

Wednesday, February 09, 2005 3:42 PM

To: Subject: O'Bryen, Barbara please search

please search nucleotides 191-220 of seq id no 1 from 09/925065 in genseq and uspats issued and published.

results on paper is fine

thanks.

Juliet Switzer Art Unit 1634

phone: 571-272-753 office: Remsen 2D75

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	146	(thiopurine with methyltransferase) or tpmt	US-PGPUB; USPAT	OR	ON	2005/02/09 15:42
L2	54	I1 same (mutation polymorphism snp)	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L3	4	I2 same intron\$3	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L4	12	(thiopurine with methyltransferase) or tpmt	DERWENT	OR	ON	2005/02/09 15:42

(FILE 'HOME' ENTERED AT 13:36:40 ON 09 FEB 2005)

12 DUP REM L7 (3 DUPLICATES REMOVED)

L8

	FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:36:48 ON 09 FEB 2005
L1	1317 S THIOPURINE (3A) METHYLTRANSFERASE
L2	928 S TPMT
L3	537 S (L1 OR L2)(4A)(POLYMORPH? OR SNP OR ALLEL?)
L4	6 S L3(6A)(INTRON?)
L5	3 DUP REM L4 (3 DUPLICATES REMOVED)
L6	FILE 'STNGUIDE' ENTERED AT 13:40:29 ON 09 FEB 2005 0 S L3 AND (ADENINE OR GUANINE)
L7	FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:19:38 ON 09 FEB 2005 15 S L6



results of BLA

BLASTN 2.2.10 [Oct-19-2004]

RID: 1107966805-21412-170660323395.BLASTQ4

Blast Sea 101 against dbSNP

Database: human snp

10,022,444 sequences: 11,321,078,719 total letters

If you have any problems or questions with the results of this search please refer to the BLAST FAQs

Taxonomy reports

No wits in prior art.

Query=

(440 letters)

Distribution of 5 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments Color Key for Alignment Scores **<40** 40-50 50-80 1_21412 8 100 150 200 250 300 350 400

Score Ε Sequences producing significant alignments: (bits) Value gnl|dbSNP|rs3925948 allelePos=205totallen=440;taxid=9606;sn... 845 0.0 gnl|dbSNP|rs13216460 allelePos=501totallen=941;taxid=9606;s... 0.0 837 gnl|dbSNP|rs2842946 allelePos=405totallen=605;taxid=9606;sn... 0.0 724 qnl|dbSNP|rs9367980 allelePos=500totallen=1000;taxid=9606;s... 587 e-165 qnl|dbSNP|rs9465101 allelePos=151totallen=512;taxid=9606;sn... 375 e - 101

Alignments

>gnl|dbSNP|rs3925948 allelePos=205totallen=440;taxid=9606;snpClass=1;alleles='A/G';m enomic;build=111 had dak Length = 440

Score = 845 bits (439), Expect = 0.0Identities = 163/440 (37%) Strand = Plus / Plus

```
caqaqaqtqtaqtqaqccaagattqtqcccctqcactccaqcqtqqqtaacaqaqtqaqa 60
Sbjct: 1
Query: 61 nnnnnnnnnnnnnnnnnnnncctattgtgaactattagtatattagtatctagagtatgt 120
                      Sbjct: 61 ctccatctaaaaaaaaaaacctattgtgaactattagtatattagtatctagagtatgt 120
Query: 121 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 180
       Sbjct: 121 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 180
Query: 181 ctaatctctgtaaatatgctctgtrtatatgctatatgctctatgttaaaggtatttgaa 240
       Sbjct: 181 ctaatctctgtaaatatgctctgtrtatatgctatatgctctatgttaaaggtatttgaa 240
Sbjct: 241 cttttctagagagatggtatatatttttttatttgtttattttttgagataggatcttgat 300
Sbjct: 301 ctgtcacccaggctggagtacagaagtgcaatcacagctcactgcagcctcgacctccct 360
Sbjct: 361 gggcacaagtgatcctcccacctcagcctcccaagtttctgggaccagaggcatgcacca 420
Query: 421 nnnnnnnnnnnnnnnnnnnc 440
Sbjct: 421 caatgcttagctaatttttc 440
>gnl|dbSNP|rs13216460 allelePos=501totallen=941;taxid=9606;snpClass=1;alleles='G/T';
       enomic;build=121
      Length = 941
Score = 837 \text{ bits } (435), \text{ Expect} = 0.0
Identities = 162/440 (36%)
Strand = Plus / Minus
Query: 1
       Sbjct: 530 cagagagtgtagtgagccaagattgtgccmctgcactccagcgtgggtaacagagtgaga 471
Query: 61 nnnnnnnnnnnnnnnnnnnnncctattgtgaactattagtatattagtatctagagtatgt 120
                     Sbjct: 470 ctccatctaaaaaaaaaacctattgtgaactattagtatattagtatctagagtatgt 411
```

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Query: 121 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 180
       Sbjct: 410 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 351
Query: 181 ctaatctctgtaaatatgctctgtrtatatgctatatgctctatgttaaaggtatttgaa 240
       Sbjct: 350 ctaatctctgtaaatatgctctgtatatatgctatatgctctatgttaaaggtatttgaa 291
Sbjct: 230 ctqtcacccaqqctqqaqtacaqaaqtqcaatcacaqctcactqcaqcctcqacctccct 171
Sbjct: 170 gggcacaagtgatcctcccacctcagcctcccaagtttctgggaccagaggcatgcacca 111
Query: 421 nnnnnnnnnnnnnnnnnn 440
Sbjct: 110 caatgcttagctaatttttc 91
>gnl|dbSNP|rs2842946 allelePos=405totallen=605;taxid=9606;snpClass=1;alleles='A/T';m
       enomic; build=119
      Length = 605
Score = 724 \text{ bits } (376), \text{ Expect = } 0.0
Identities = 160/378 (42%)
Strand = Plus / Minus
Query: 63 nnnnnnnnnnnnnnnnncctattgtgaactattagtatattagtatctagagtatgtct 122
                   Sbjct: 605 ccatctaaaaaaaaaacctattgtgaactattagtatattagtatctagagtatgtct 546
Query: 123 ataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaact 182
       Sbjct: 545 ataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaact 486
Query: 183 aatctctgtaaatatgctctgtrtatatgctatatgctctatgttaaaggtatttgaann 242
       Sbjct: 485 aatctctgtaaatatgctctgtatatatgctatatgctctatgttaaaggtatttgaact 426
Sbjct: 425 tttctagagagatggtatatwtttttttatttgtttatttttgagataggatcttgatct 366
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Sbjct: 365 gtcacccaggctggagtacagaagtgcaatcacagctcactgcagcctcgacctccctgg 306
Sbjct: 305 gcacaagtgatcctcccacctcagcctcccaagtttctgggaccagaggcatgcaccaca 246
Query: 423 nnnnnnnnnnnnnnnn 440
Sbjct: 245 atgcttagctaatttttc 228
>gnl|dbSNP|rs9367980 allelePos=500totallen=1000;taxid=9606;snpClass=1;alleles='A/C';
       nomic; build=121
      Length = 1000
Score = 587 \text{ bits } (305), \text{ Expect} = e-165
Identities = 109/309 (35%)
Strand = Plus / Minus
Query: 132
       aaaagataaagaccattttattgaaagttgttttatcttagaaaaggaactaatctctgt 191
       Sbjct: 1000 aaaagataaagaccattttattgaaagttgttttatcttagaaaaggaactaatctctgt 941
Query: 192
       Sbjct: 940
       aaatatgctctgtatatatgctatatgctctatgttaaaqqtatttqaacttttctaqaq 881
Query: 252
       Sbjct: 880
       Sbjct: 820
       gctggagtacagaagtgcaatcacagctcactgcagcctcgacctccctqqqcacaaqtq 761
Sbjct: 760 atcctcccacctcagcctcccaagtttctgggaccagaggcatgcaccacaatgcttagc 701
Query: 432
       nnnnnnnc 440
Sbjct: 700
       taatttttc 692
```

>gnl|dbSNP|rs9465101 allelePos=151totallen=512;taxid=9606;snpClass=1;alleles='A/T';m

enomic; build=119

```
Length = 512
 Score = 375 \text{ bits } (195), \text{ Expect} = e-101
 Identities = 121/199 (60%)
 Strand = Plus / Minus
          Query: 1
Sbjct: 199 cagagagtgtagtgagccaagattgtgccactgcactccagcgtgggtwacagagtgaga 140
Query: 61 nnnnnnnnnnnnnnnnnnncctattgtgaactattagtatattagtatctagagtatgt 120
                            Sbjct: 139 ctccatctaaaaaaaaaacctattgtgaactattagtatattagtatctagagtatgt 80
Query: 121 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 180
          Sbjct: 79 ctataaaatttaaaagataaagaccattttattgaaagttgttttatcttagaaaaggaa 20
Query: 181 ctaatctctgtaaatatgc 199
          111111111111111111
Sbjct: 19 ctaatctctgtaaatatgc 1
Lambda
         K
                Н
         0.621
   1.33
                    1.12
Gapped
Lambda
          K
   1.33
          0.621
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 10022444
Number of Hits to DB: 6981
Number of extensions: 0
Number of successful extensions: 0
Number of sequences better than 1.0e-02: 0
Number of HSP's better than 0.0 without gapping: 0
Number of HSP's gapped: 0
Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 0.0: 0
Length of query: 440
Length of database: 11,321,078,719
Length adjustment: 25
Effective length of query: 415
Effective length of database: 11,070,517,619
Effective search space: 4594264811885
Effective search space used: 4594264811885
X1: 13 (25.0 bits)
X2: 31 (60.0 bits)
X3: 25 (50.0 bits)
S1: 13 (25.0 bits)
```

S2: 25 (48.8 bits)